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SEQUENCE LISTING

<110> Ford, John
Mulero, Julio

<120> METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
POLYPEPTIDES

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<150> PCT/US99/16180

<151> 1999-07-16

<150> 09/350,836

<151> 1999-07-09

<150> 09/273,447

<151> 1999-03-19

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<151> 1999-02-04

<150> 09/122,449

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<170> PatentIn Ver. 2.0

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gcaggtgtgc gagcaggatt gcttctgcaa caaaagcctc caccagcca catcttgga 240
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Cys Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu
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Gly Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr
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Leu Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His
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gtt tac acc ttt gtg cag aaa atg cca gga cag ctt cca att cta gaa 482
Val Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu
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ggg gaa gtt ttt gat tct gtg aag cca gga ctt tct gct ttt gta gat 530
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caa cct aag cag ggt gct gag acc gtt caa ggg ctc tta gag gtg gcc 578
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His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu	
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Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala	
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Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys	
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 Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
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 Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
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 Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
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 Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
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 Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
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gac Asp	tca Ser	atc Ile 115	ccc Pro	cga Arg	agt Ser	cac His	tgg Trp 120	aaa Lys	aag Lys	acc Thr	cca Pro	gtg Val 125	gtc Val	cta Leu	aag Lys	384
gca Ala	aca Thr 130	gca Ala	gga Gly	cta Leu	cgc Arg	tta Leu 135	ctg Leu	cca Pro	gaa Glu	cac His 140	aaa Lys 140	gcc Ala	aag Lys	gct Ala	ctg Leu	432
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tta Leu	ccg Pro 275	aga Arg	tgg Trp	ttg Leu	gaa Glu	gca Ala	gag Glu 280	tgg Trp	atc Ile	ttt Phe	ggg Gly 285	ggg Gly 285	gtg Val	aaa Lys	tac Tyr	864
cag Gln 290	tat Tyr	ggg Gly	ggc Gly	aac Asn	caa Gln	gaa Glu 295	ggg Gly	gag Glu	gtg Val	ggc Gly 300	ttt Phe 300	gag Glu	ccc Pro	tgc Cys	tat Tyr	912

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Leu	Pro	Arg	Trp	Leu	Glu	Ala	Glu	Trp	Ile	Phe	Gly	Gly	Val	Lys	Tyr	
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acaaagccaa ggctctgctc tttgaggtaa aggagatctt caggaagtca ctttctctgg 720
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<213> Homo sapiens

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          20             25             30

Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
    35             40             45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
    50             55             60

Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
    65             70             75             80

Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
          85             90             95

Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
    100             105             110

Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
    115             120             125

Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
    130             135             140

Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro
    145             150             155             160

Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala
          165             170             175

Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln
    180             185             190

Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
    195             200             205

Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
    210             215             220

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Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
225 230 235 240
Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly
245 250 255
Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys
260 265 270
Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr
275 280 285
Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr
290 295 300
Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu
305 310 315 320
Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala
325 330 335
Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val
340 345 350
Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn
355 360 365
Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr
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<212> DNA

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gcgcggtgca tggaatgggc tatgtga atg aaa aaa ggt atc cgt tat gaa act 174
Met Lys Lys Gly Ile Arg Tyr Glu Thr
1 5

tcc aga aaa acg agc tac att ttt cag cag ccg cag cac ggt cct tgg 222
Ser Arg Lys Thr Ser Tyr Ile Phe Gln Gln Pro Gln His Gly Pro Trp
10 15 20 25

caa aca agg atg aga aaa ata tcc aac cac ggg agc ctg cgg gtg gcg 270
Gln Thr Arg Met Arg Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala
30 35 40

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Lys	Val	Ala	Tyr	Pro	Leu	Gly	Leu	Cys	Val	Gly	Val	Phe	Ile	Tyr	Val	
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gcc	tac	atc	aag	tgg	cac	cgg	gcc	acc	gcc	acc	cag	gcc	ttc	ttc	agc	366
Ala	Tyr	Ile	Lys	Trp	His	Arg	Ala	Thr	Ala	Thr	Gln	Ala	Phe	Phe	Ser	
		60					65					70				
atc	acc	agg	gca	gcc	ccg	ggg	gcc	cgg	tgg	ggg	cag	cag	gcc	cac	agc	414
Ile	Thr	Arg	Ala	Ala	Pro	Gly	Ala	Arg	Trp	Gly	Gln	Gln	Ala	His	Ser	
	75					80					85					
ccc	ctg	ggg	aca	gct	gca	gac	ggg	cac	gag	gtc	ttc	tac	ggg	atc	atg	462
Pro	Leu	Gly	Thr	Ala	Ala	Asp	Gly	His	Glu	Val	Phe	Tyr	Gly	Ile	Met	
90					95					100					105	
ttt	gat	gca	gga	agc	act	ggc	acc	cga	gta	cac	gtc	ttc	cag	ttc	acc	510
Phe	Asp	Ala	Gly	Ser	Thr	Gly	Thr	Arg	Val	His	Val	Phe	Gln	Phe	Thr	
				110					115					120		
cgg	ccc	ccc	aga	gaa	act	ccc	acg	tta	acc	cac	gaa	acc	ttc	aaa	gca	558
Arg	Pro	Pro	Arg	Glu	Thr	Pro	Thr	Leu	Thr	His	Glu	Thr	Phe	Lys	Ala	
			125					130					135			
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Val	Lys	Pro	Gly	Leu	Ser	Ala	Tyr	Ala	Asp	Asp	Val	Glu	Lys	Ser	Ala	
		140					145					150				
cag	gga	atc	cgg	gaa	cta	ctg	gat	gtt	gct	aaa	cag	gac	att	ccg	ttc	654
Gln	Gly	Ile	Arg	Glu	Leu	Leu	Asp	Val	Ala	Lys	Gln	Asp	Ile	Pro	Phe	
	155					160					165					
gac	ttc	tgg	aag	gcc	acc	cct	ctg	gtc	ctc	aag	gcc	aca	gct	ggc	tta	702
Asp	Phe	Trp	Lys	Ala	Thr	Pro	Leu	Val	Leu	Lys	Ala	Thr	Ala	Gly	Leu	
170					175					180					185	
cgc	ctg	tta	cct	gga	gaa	aag	gcc	cag	aag	tta	ctg	cag	aag	gtg	aaa	750
Arg	Leu	Leu	Pro	Gly	Glu	Lys	Ala	Gln	Lys	Leu	Leu	Gln	Lys	Val	Lys	
			190						195					200		
gaa	gta	ttt	aaa	gca	tcg	cct	ttc	ctt	gta	ggg	gat	gac	tgt	gtt	tcc	798
Glu	Val	Phe	Lys	Ala	Ser	Pro	Phe	Leu	Val	Gly	Asp	Asp	Cys	Val	Ser	
			205					210					215			
atc	atg	aac	gga	aca	gat	gaa	ggc	gtt	tcg	gcg	tgg	atc	acc	atc	aac	846
Ile	Met	Asn	Gly	Thr	Asp	Glu	Gly	Val	Ser	Ala	Trp	Ile	Thr	Ile	Asn	
		220					225					230				
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Phe	Leu	Thr	Gly	Ser	Leu	Lys	Thr	Pro	Gly	Gly	Ser	Ser	Val	Gly	Met	
	235					240					245					
ctg	gac	ttg	ggc	gga	gga	tcc	act	cag	atc	gcc	ttc	ctg	cca	cgc	gtg	942
Leu	Asp	Leu	Gly	Gly	Gly	Ser	Thr	Gln	Ile	Ala	Phe	Leu	Pro	Arg	Val	
250					255					260					265	
gag	ggc	acc	ctg	cag	gcc	tcc	cca	ccc	ggc	tac	ctg	acg	gca	ctg	cgg	990
Glu	Gly	Thr	Leu	Gln	Ala	Ser	Pro	Pro	Gly	Tyr	Leu	Thr	Ala	Leu	Arg	
				270					275					280		

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Met Phe Asn Arg Thr Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu	
285 290 295	
ggg ctg atg tcg gca cgc ctg gcg atc ctg ggc ggc gtg gag ggg cag	1086
Gly Leu Met Ser Ala Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln	
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cct gct aag gat gga aag gag ttg gtc agc cct tgc ttg tct ccc agt	1134
Pro Ala Lys Asp Gly Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser	
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ttc aaa gga gag tgg gaa cac gca gaa gtc acg tac agg gtt tca ggg	1182
Phe Lys Gly Glu Trp Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly	
330 335 340 345	
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Gln Lys Ala Ala Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser	
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gag gtc ctt caa aac aga gtg cac agg acg gag gaa gtg aag cat gtg	1278
Glu Val Leu Gln Asn Arg Val His Arg Thr Glu Glu Val Lys His Val	
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Asp Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly	
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ctc ata gat gcg gag aag gga ggc agc ctg gtg gtg ggg gac ttc gag	1374
Leu Ile Asp Ala Glu Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu	
395 400 405	
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Ile Ala Ala Lys Tyr Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser	
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Ser Pro Phe Ser Cys Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln	
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Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro Leu Gly
          35           40           45
Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp His Arg
      50           55           60
Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala Pro Gly
  65           70           75           80
Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala Ala Asp
          85           90           95
Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly
          100           105           110
Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu Thr Pro
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Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu Ser Ala

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Ala Gln Lys 195	Leu Leu Gln Lys Val 200	Glu Val Phe Lys 205
Ala Ser Pro		
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Gly 225	Val Ser Ala Trp Ile 230	Thr Ile Asn Phe Leu 235
Thr Pro Gly Gly Ser 245	Ser Val Gly Met Leu 250	Asp Leu Gly Gly Gly Ser 255
Thr Gln Ile Ala 260	Phe Leu Pro Arg Val 265	Glu Gly Thr Leu Gln 270
Ala Ser		
Pro Pro Gly 275	Tyr Leu Thr Ala Leu 280	Arg Met Phe Asn Arg 285
Thr Tyr Lys		
Leu Tyr 290	Ser Tyr Ser Tyr Leu 295	Gly Leu Gly Leu Met 300
Ser Ala Arg Leu		
Ala 305	Ile Leu Gly Gly Val 310	Glu Gly Gln Pro Ala 315
Lys Asp Gly Lys Glu 320		
Leu Val Ser Pro Cys 325	Leu Ser Pro Ser Phe 330	Lys Gly Glu Trp Glu 335
His		
Ala Glu Val Thr 340	Tyr Arg Val Ser Gly 345	Gln Lys Ala Ala Ala 350
Ser Leu		
His Glu 355	Leu Cys Ala Ala Arg Val 360	Ser Glu Val Leu Gln 365
Asn Arg Val		
His Arg 370	Thr Glu Glu Val Lys 375	His Val Asp Phe Tyr 380
Ala Phe Ser Tyr		
Tyr 385	Tyr Asp Leu Ala Ala 390	Gly Val Gly Leu Ile 395
Asp Ala Glu Lys Gly 400		
Gly Ser Leu Val Val 405	Gly Asp Phe Glu Ile 410	Ala Ala Lys Tyr Val 415
Cys		
Arg Thr Leu Glu 420	Thr Gln Pro Gln Ser 425	Ser Pro Phe Ser Cys 430
Met Asp		
Leu Thr Tyr Val Ser Leu Leu 440	Leu Gln Glu Phe Gly Phe 445	Pro Arg Ser
Lys Val 450	Leu Lys Leu Thr Arg 455	Lys Ile Asp Asn Val 460
Glu Thr Ser Trp		

- 29 -

Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg Gln Lys
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Ser Pro Ala Ser

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<220>
<223> Description of Artificial Sequence: primer

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<220>
<223> Description of Artificial Sequence: primer

<400> 31
tgaagtcacg tccaggacag g 21

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<220>
<223> Description of Artificial Sequence: primer

- 30 -

<400> 32
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<210> 33
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<220>
<223> Description of Artificial Sequence: .primer

<400> 33
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<210> 34
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oligonucleotide primer

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<210> 37
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- 31 -

oligonucleotide primer

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21